



1 CCCCTGGAC AGCCGCCCTC TCCITCAGGC CCGTGGGGCT GGCCCTGCAC CGCCGAGCTT CCGGGGATGA GGGCCCCCGG TGTGTCACC CGGCGCGGCC  
GGGGACCTG TCGGCGGGAG AGGAGGTCCG GGCACCCGGA CCGGGACGTG GCGGCTCGAA GGGCCCTACT CCGGGGGGCC ACACCACTGG GCGCGCGCGG

101 CAGGTGCTG AGGAGCCCG GCCAGCCCG GAGATGGGG IGCACGTGA GTACTCGCG GCTGGGCGCT CCGCCCGGCC CGGTCCCTG TTTGAGCGGG  
GTCCAGGAC TCCCTGGGG CCGTCCCGC CTCTACCCC ACGTCCACT CATGACGCC CGACCCGCGA GGGCGGGCGG GCCACGGAC AAACCTCGGCC  
1 M G V H  
^Exon 1  
^Met 1

201 GATTAGCG CGGGCTATT GGCCGGGAGG TGGTGGGT CAAGGACCG CGACTTGTA AGGACCCCG AGGGGGAGG GGGTGGGG AGCCTCCACG  
CTAAATCGG GGCCGATAA CCGGCCCTCC ACCGACCAA GTTCTGGCC GCTGAACAGT TCTGGGGCC TTCCCTCTCC CCCCACCCG TCGGAGGTGC

301 TGCCAGCGG GACTTGGGG AGTCTTGGG GATGGCAAAA ACCTGACCTG TGAAGGGG ACAGTTGGG GGTGAGGG AGAAGGTTT GGGGTCTG  
ACGGTCGCC CTGAACCCCC TCAGGAACCC CTACCGTTT TGGACTGGAC ACTTCCCTG TGTCAAACCC CCAACTCCCC TTCTCCAA CCCCCAAGC

401 CTGTGCCAST GGAGAGGAAG CTGATAAGCT GATAACCTGG GCGTGGAG CACCATTAT CTGCAGAGG GNNNTGTA GCTGGGGTG GGGTGTGAC  
GACACGTS A CCTCTCTC GACTATTGTA CTATTGACC CCGGACCTCG GTGGTAATA GACGCTCTCC CNNNNACCAT CGACCCCCAC CCAACACGTG

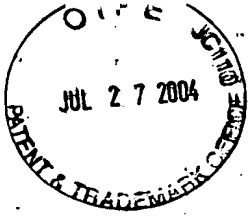
501 ACGGAGCAG GATTGAATGA AGGCAGGGA GGCAGCACCT GAGTGTTC ATGTTGGG ACAGGAAGGA CGAGCTGGG CAGACACGTG GGGATGAAGG  
TGCGTCGT CTAACCTACT TCCGTCCCT CCGTCCGTGA CTCAGAACG TACCAACCCC TGTCCTTCT GTCGACCCC GTCTCTGCAC CCCTACTTCC

601 AAGCTGTCT TCCACAGCCA CCCTTCTCCC TCCCGCCCTG ACTCTAGCC TGGTATCTC TTCTAGAAIG TCCTGCCIG CIGTGGCTIC ICCGTCCCT  
TTGACAGGA AGGTGTCGT GGAAGAGG AGGGCGGAC TGAGAGTCG ACCGATAGG AAGATCTTAC AGGACGGACC GACACCGAAG AGGACAGGA  
1 E C P A W L W L L L S L  
^Exon 2

701 GCTGTCGCT CCTCTGGCC TCCAGTCTT GGGGCCCCCA CCAGCCCTCA TCTGTGACG CCGATCTTG GAGAGTACC TCTGGAGG CAAGGAGGCC  
CGACAGGAG GGAGACCCG AGGTACGA CCGCGGGGT GGTGGGAGT AGACACTGTC GGTCTAGGAC CTCTCCATGG AGAACCCTCG GTTCTCCGG  
13 L S L P L G L P V L G A P P R L I C D S R V L E R Y L L E A K E A

801 GAGATATCA CGGTGAGACC CCTTCCCCAG CACATTCCAC AGAATCAG CTCAGGGCTT CAGGGAATC CTCCAGATC CAGGAACCTG GCACTTGGT  
CTCTATAGT GCCACTCTG GGAAGGGGTC GTGAAGGTG TCTTGAGTG GAGTCCGAA GTCCCTTGA GAGGGTCTAG GTCCTTGGAC CCGTAACCA  
46 E N I T

FIG. 1A



901	TGGGGTGGAG ACCCACCTC	TTGGGAAGCT AACCCTTCGA	AGACACTGCC TCTGTGACGG	CCCTACATA GGGGATGAT	AGATAAGTC TCTTATTGAG	TGGTGGCCCC ACCAACGGGG	AAACCATACC TTTGGTATGG	TGAAACTAG ACCTTTGATC	GCAAGGAGCA CGTTCCTCGT	AAGCCAGCAG TTCGGTCTGC
1001	ATCCTAGGCG TAGGATGCCG	CTGTGGGCCA GACACCCGGT	GGGCCAGAGC CCCGGTCCTG	CTTCAGGAC GAAGTCCCTG	CCTTGACTCC GGAACGTGAG	CCGGGCTGTG GGCCCGACAC	TGCATTTGAG ACGTAAATGC	ACGGGCTGTG TGCCCGACAC	CCGAACACTG GGCTTGTGAC	CAGCTTGAAT GTGGAACCTA
1						T G C A ^ exon 3			E H C	S L N
1101	GAGAAATATCA CTCTTATAGT	CTGTCCCGAG GACAGGGTCT	CACCAAGTT GTGGTTTCAA	AATTTCATG TTAAAGATAC	CCTGGAAGAG GGACTTCTC	GATGAGGTG CTACCTCCAC	AGTTCCTTTT TCAAGGAA	TTTTTTTTTT AAAAAANA	TCCTTTCTTT AGGAAAGAAA	TGAGAAATCT ACCTCTTAGA
11	E N I T	V P D	T K V	N F Y A	W K R	M E				
1201	CATTGGAG GTAAACGCTC	CCTGATTTG GGACTAANAAC	GATGAAGGT CTACTTTCCC	AGAATGATCG TCTTACTAGC	AGGGAAGGT TCCCTTTCCA	AAATGGAGC TTTTACCTCG	AGCAGAGATG TCGTCTCTAC	AGGTGCTCTG TCCGACGGAC	GGCGCAGAGG CCGCGTCTCC	CTCACGTCTA GAGTGCAGAT
1301	TAATCCAGG ATTAGGGTCC	CTGAGATGGC GACTCTACCG	CGAGATGGGA GCTCTACCTT	GAATGCTGTG CTTAAGGAAC	AGCCCTGGAG TCGGGACCTC	TTTTAGACCA AAAGTCTGGT	ACCTGGGAG TGGAACCGTC	CATAGTGAGA GTATCACTCT	TCCCCCATCT AGGGGGTAGA	CTACAAACAT GATGTTTGTA
1401	TTAAAAAAT AATTTTTTTA	TAGTCAGGTG ATCAGTCCAC	AGTGGGTGCA TCCACCAGGT	TGGTGGTAGT ACCACCATCA	CCCAGATATT GGGTCTATAA	TGGAAGGCTG ACCTTCCGAC	AGGCGGGAGG TCCGCCCTCC	ATCGCTTGAG TAGCGAACTC	CCCAGGAATT GGTCTCTTAA	TGAGGCTGCA ACTCCGAGGT
1501	GTGAGCTGTG CACTCGACAC	ATCACACCAC TAGTGTGGTG	TGCATCCGAG ACGTGAGGTC	CCTCAGTGAC GGAGTCACTG	AGAGTGAGGC TCTCACTCCG	CCTGTCTCAA GGACAGAGTT	AAAAGAAAG TTTTCTTTC	AAAAAAGAAA TTTTTTTTTT	AATAATGAGG TTATTACTCC	GCTGTATGGA GCACATACCT
1601	ATACATTCAT TATGTAAGTA	TATTCATTCA ATAAGTAAGT	CTCACTCATT GAGTGAGTAA	CATTCAATCA GTAAATAGT	TTCAATTCNN AAGTAAGNN	NNNTCTTATT NNNAGATTA	GCATACCTCT CGTATGGAGA	GTTTGTCTCAG CAAAGAGTC	CTTGGTGTCT GAACCAAGAA	GGGGCTGCTG CCCCGACGAC
1701	AGGGCAGGA TCCCCGTCTT	GGGAGAGGT CCCTCTCCCA	GGCATGGGTC CCGTACCCAG	AGCTGACTCC TCGACTGAGG	CAGAGTCCAC GTCTCAGGTG	TCCTGTAGG AGGGACATCC	TCAGGCGAGCA AGTCCGTGCT	GGCCGTAGAA CCGGCATCTT	GTCTGGCAGG CAGACCGTCC	GCCTGGCCCT CCGACCCGGA
1						V ^	R Q Q	A V E	V W Q G	L A L
1801	GCTCTCGGA CGAGAGCCTT	GCTGTCTGCT CGAGAGGACG	GGGGCCAGGC CCCCGTCCG	CCTGTGCTC GGACAAACAG	AATCTTCCC TTGAGAGGG	AGCCGTGGGA TGGCACCTT	GCCCTGCGAG CGGGGACGTC	CTGCATGTGG GACGTACACC	ATAAGCCGT TATTTCCGCA	CAGTGGCCTT GTCACCCGAA
15	L S E	A V L R	G Q A	L L V	N S S Q	P W E	P L Q	L H V D	K A V	S G L
1901	CGAGCCTCA GGTTCGGAGT	CCACTCTGCT GGTGAGACGA	TGGGCTCTG AGCCCGAGAC	GGAGCCACAG CCTCGGTCC	TGAGTAGGAG ACTCATCTC	CGACACTTC GCTGTGAG	TGCTTCCCT ACGAACGGGA	TTCTGTGAAGA AAGACATCT	AAGGGAGAAG TTCCCTCTTC	GGTCTTGTCTA CCAGAACGAT
48	B S I T	T L L	B A L	G A O						

FIG. 1B



2001 AGGAGTACAG GAACGTGICCG TATTCCTTCC CCTTCTGTGG CACTGCAGCG ACCTCCTGTT TTCTCCTTGG CAGAAGGAAG CCATCTCCCC TCCAGATGCG  
TCCTCATGTC CTTGACAGGC ATAAGGAAGG GGAAGACACC GTGACGTGCG TGGAGGACAA AAGAGAACCC GTCTTCTTTC GGTAGAGGGG AGGTCTACCG  
1 K E A I S P P D A  
^exon 5  
2101 GCCTCAGCTG CTCCACTCCG AACAATCACT GCTGACACTT ICCGCAACT CTTCGAGTC TACICCAATT TCCTCGCGG AAAGCTGAAG CTGTACACAG  
CGGAGTCGAG GAGGTGAGGC TTGTTAGTGA CGACTGTGAA AGCGTTTGA GAAGGCTCAG ATGAGGTAA AGGAGGCCCG TTTCGACTTC GACATGTGTC  
10 A S A A P L R T I T A D T F R K L F R V Y S N F L R G K L K L Y T G  
2201 GGGAGGCCCTG CAGGACAGGG GACAGATGAC CAGGTGTGTC CACTGGGCA TATCCACCAC CTCCTCACC AACATTGCTT GTGCCACACC CTCCTCCGCG  
CCCTCCGGAC GTCTGTGCCC CTGTCTACTG GTCCACACAG GTGGACCCGT ATAGTGGTG GAGGGAGTGG TTGTAACGAA CACGGTGTGG GAGGGGGGGG  
44 E A C R T G D R O  
2301 ACTCCTGAAC CCCGTCGAGG AGCTCTCAG  
TGAGGACTTG GGGCAGCTCC TCGAGAGTC

FIG. 1C



1	ATGGGGTGC	ACGAATGTC	TGCTTCTCC	TGCTCTGCT	GTGCTCCCT	CTGGGCTCC	CAGTCCTGGG	CGCCCCACCA	CGCTCATCT
1	TACCCACAG	TGCTTACAG	ACCGAAGAG	ACAGGACGA	CAGCGAGGA	GACCGGAGG	GTCAGGACCC	CGCGGTGGT	CGCGAGTAG
	M G V H	E C P	W L L L	S L L	S L P	L G L P	V L G	A P P	R L I C
101	GTGACAGCG	AGTCTGGAG	TGGAGGCCAA	GGAGGCCGAG	AATATCACGA	CGGCTGTGC	CGAACACTGC	AGCTTGAATG	AGAATATCAC
35	CACTGTCCG	TCAGGACCTC	ACCTCCGTT	CCTCCGCTC	TTATAGTGT	GCCGACACG	GCTGTGTGAG	TCGAACCTTAC	TCTTATAGTG
	D S R	V L E	E A K	E A E	N I T T	G C A	E H C	S L N E	N I T
									*
201	TGTCCAGAC	ACCAAAGTTA	CTGGAAGAG	ATGGAGTCA	GGCAGCAGG	CGTAGAAGTC	TGGCAGGGCC	TGGCCCTGCT	CTCGGAAGCT
68	ACAGGGTCTG	TGGTTTCAAT	GACCTTCTCC	TACCTCCAGT	CCGTGTCCG	GCATCTTCAG	ACCGTCCCG	ACCGGACGA	GAGCCTTCGA
	V P D	T K V N	W K R	M E V R	Q Q A	V E V	W Q G L	A L L	S E A
301	GTCCTGCGG	GCCAGGCCCT	TCTTCCAGC	CGTGGAGCC	CCTGCAGCTG	CATGTGGATA	AAGCCGTGAG	TGGCCTTCCG	AGCCTCACCA
101	CAGGACGCC	CGGTCCGGA	AGAGGGTCG	GCACCTCGG	GGAGTTCGAC	GTACACCTAT	TTCGGCAGTC	ACCGGAAGCG	TCGGAGTGT
	V L R G	Q A L	S S Q P	W E P	L Q L	H V D K	A V S	G L R	S L T T
401	CTCTGCTTCG	GGCTCTGGGA	GGCTTCTCC	CCCTCCAGAT	CGGGCTCAG	CTGCTCCACT	CCGAACAATC	ACTGCTGACA	CTTTCGCAA
135	GAGACGAGC	CCGAGACCT	TTCGGTAGAG	GGGAGTCTA	CGCCGAGTC	GACGAGGTGA	GGCTTGTAG	TGACGACTGT	GAAAGGCGTT
	L L R	A L G	A I S	P P D	A A S A	A P L	R T I	T A D T	F R K
501	ACTCTTCCGA	GTCTACTCCA	GTCTTCTCC	AGCTGTACA	CAGGGAGGC	CTGCAGGACA	GGGACAGAT	GACCA	
148	TGAGAAGCT	CAGATGAGGT	CCCTTTCGAC	TTGACATGT	GTCCCTCCG	GACCTCCTGT	CCCCTGTCTA	CTGGT	
	L F R	V Y S N	G K L	K L Y T	G E A	C R T	G D R O		

FIG.2

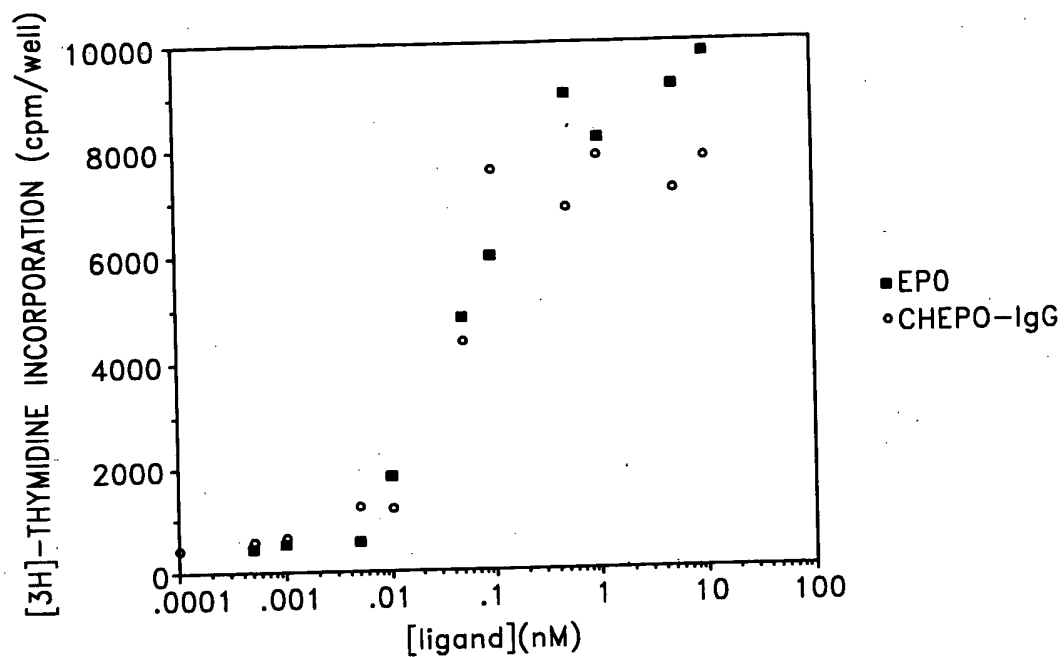


HUMAN	MGVHECPAWLWLLSLLSLPLGLPVLGAPPRILICDSRVLYLLEAKEAE *****
CHEPO	MGVHECPAWLWLLSLLSLPLGLPVLGAPPRILICDSRVLYLLEAKEAE *****
HUMAN	NITGCAEHCSLNENITVPTKVNFYAWKRMEVGQQAQVEVWQLALLSEA *****
CHEPO	NITGCAEHCSLNENITVPTKVNFYAWKRMEVGQQAQVEVWQLALLSEA *****
HUMAN	VLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAISPPD *****
CHEPO	VLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAISPPD *****
HUMAN	AASAAPLRITITADTFRKLFrvysNfLrGKlKlYtGEACRTGDR *****
CHEPO	AASAAPLRITITADTFRKLFrvysNfLrGKlKlYtGEACRTGDR *****

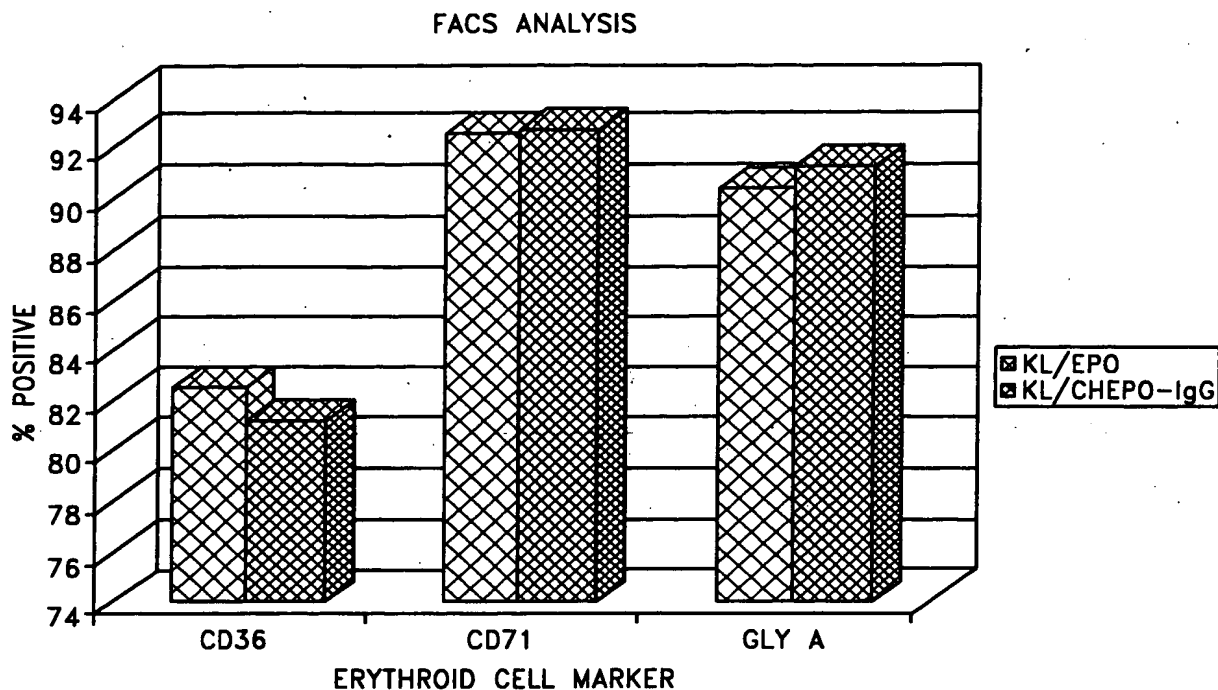
**FIG.3**



Application No.: 09/813,775  
Filing Date: March 20, 2001  
Title: Novel Chimpanzee Erythropoietin  
(CHEPO) Polypeptides...  
Docket No.: 39755-0057 CP2  
Sheet 6 of 7



**FIG. 4**



**FIG.5**